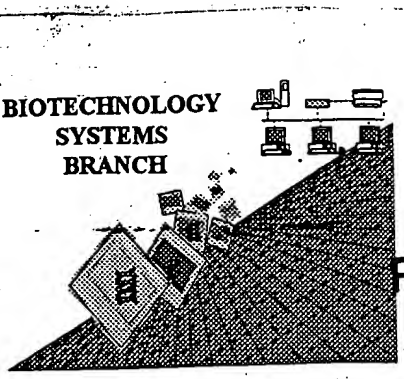
Follow

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/251,133

Source: 1642

Date Processed by STIC: 9/20/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/251,133

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 J Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

A. Holleran

#8 AM 9/27/00

1642

RAW SEQUENCE LISTING DATE: 09/20/2000
PATENT APPLICATION: US/09/251,133 TIME: 16:21:27

Input Set : A:\Kumed15
Output Set: N:\CRF3\09202000\I251133.raw

Does Not Comply
Corrected Diskette Needed

```
  3 <110> APPLICANT: SHAH, Girish V.
  5 <120> TITLE OF INVENTION: NEUROENDOCRINE MARKER OF PROSTATE CANCER AND METHOD FOR
  6       PRODUCING SAME
  8 <130> FILE REFERENCE: 70009590-015
 10 <140> CURRENT APPLICATION NUMBER: 09/251,133
 11 <141> CURRENT FILING DATE: 1999-02-16
 13 <150> PRIOR APPLICATION NUMBER: US 60/074,809
 14 <151> PRIOR FILING DATE: 1998-02-17
 16 <160> NUMBER OF SEQ ID NOS: 12
 18 <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

```
 97 <210> SEQ ID NO: 3
 98 <211> LENGTH: 433
 99 <212> TYPE: DNA
100 <213> ORGANISM: Homo sapien
102 <400> SEQUENCE: 3
103 agaacctgtg tgctgggcta cctgcatata gtgccagagt tcatcgaatc tcagctgctg 60
104 gggctcctta gtcctgtttc actttaacca tatgcaagac attcctcaac gttataggca 120
105 agtagactgc atcttttttt ttctttttct ttctttttct tttttctttt tttcggagct 180
106 ggggaccgaa cccaggacct tgcgcttgct aggcaagcgc tctaccactg agctaaatcc 240
E--> 107 caaccccgac tgcatcgttt ttggttttta gttaaattcc ggtttgctct atttcgtgt0 300
E--> 108 tccctttgtt taaaagaaac tgtagccggg gtagtatatg tctataatcc cagcagttgg 360
E--> 109 gaggcaggag gatccagagt tcaagtcggc atggcacaca tgagacatta gctcaaaaaa 420
E--> 110 aaaaaaaaaa aaa 433
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 435
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapien
134 <400> SEQUENCE: 5
135 attagaacct gtgtgctggg ctacctgcat atagtgccag agttcatcga atctcagctg 60
136 ctggggctcc ttagtcctgt ttcctttaac catatgcaag acattcctca acgttatagg 120
137 caagtagact gcatcttttt ttttcttttt ttttcttttt ctttttttctt tttttcggag 180
138 ctggggaccg aacccaggac cttgcgcttg ctaggcaagc gctctaccac tgagctaaat 240
139 gcccaacccc gactgcatcg tttttggttt ttagttaaat tccggtttgc tctatttcgt 300
E--> 140 0gttcccttt gtttaaaaga aactgtagcc ggggtagtat atgtctataa tcccagcagt 360
E--> 141 tgggaggcag gaggatccag agttcaagtc ggcatggcac acatgagaca ttagctcaaa 420
E--> 142 aaaaaaaaaa aaaaa 435
183 <210> SEQ ID NO: 9
184 <211> LENGTH: 103
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapien
188 <400> SEQUENCE: 9
189 Arg Thr Cys Val Leu Gly Tyr Leu His Ile Val Pro Glu Phe Ile Glu
190   1               5                  10                  15
```

see next page

invalid base (nucleic acid designator)

nos. off, as a result of above error

invalid

numbering off

RAW SEQUENCE LISTING DATE: 09/20/2000
PATENT APPLICATION: US/09/251,133 TIME: 16:21:27

Input Set : A:\Kumed15
Output Set: N:\CRF3\09202000\I251133.raw

```
     192 Ser Gln Leu Leu Gly Leu Leu Ser Pro Val Ser Phe Asn His Met Gln
     193              20                  25                  30
     195 Asp Ile Pro Gln Arg Tyr Arg Gln Val Asp Cys Ile Phe Phe Phe Leu
     196          35                  40                  45
     198 Phe Phe Ser Phe Ser Phe Phe Phe Phe Ser Glu Leu Gly Thr Glu Pro
E--> 199      50  50              55                  60
     201 Arg Thr Leu Arg Leu Leu Gly Lys Arg Ser Thr Thr Glu Leu Asn Pro
E--> 202 65                  70  70              75  75                  80  80
     204 Gln Pro Arg Leu His Arg Phe Trp Phe Leu Val Lys Phe Arg Phe Ala
E--> 205          85  85          90  90              95  95
     207 Leu Phe Arg Val Pro Phe Val
E--> 208              100  100
```

mesaligned amino acid nos. (see item 4 on Error Summary Sheet)

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 09/20/2000
PATENT APPLICATION: US/09/251,133 TIME: 16:21:28

Input Set : A:\Kumed15
Output Set: N:\CRF3\09202000\I251133.raw

L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:107 M:254 E: No. of Bases conflict, LENGTH:Input:300 Counted:299 SEQ:3
M:254 Repeated in SeqNo=3
L:110 M:252 E: No. of Seq. differs, <211>LENGTH:Input:433 Found:432 SEQ:3
L:140 M:254 E: No. of Bases conflict, LENGTH:Input:360 Counted:359 SEQ:5
L:140 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:254 Repeated in SeqNo=5
L:142 M:252 E: No. of Seq. differs, <211>LENGTH:Input:435 Found:434 SEQ:5
L:199 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9